

SEQUENCE LISTING

<110> Paul O. Sheppard
Si Lok

<120> Mammalian Secretory Protein Zsig43

<130> 98-15C1

<150> 60/109,915

<151> 1998-11-23

<150> 09/440,484

<151> 1999-11-15

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<212> DNA

<213> Homo sapiens

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<221> CDS

222 (18) . . . (2495)

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ccc ggc aag tcg ccg gag ccc ccc agc ccg cag gag atc ctg atc 146
 Pro Gly Lys Ser Pro Pro Glu Pro Pro Ser Pro Gln Glu Ile Leu Ile
 30 35 40

aag gtg caq gtg tat gtg agc ggg qaq ctg gtg ccc ctg qcc cgg qcc 194

Lys Val Gln Val Tyr Val Ser Gly Glu Leu Val Pro Leu Ala Arg Ala			
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tca gtg gat gtg ttt ggg aac cgg act ctg ctg gca gct ggc acc aca			242
Ser Val Asp Val Phe Gly Asn Arg Thr Leu Leu Ala Ala Gly Thr Thr			
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gac tca gag ggt gtg gcc acc ctg ccc ctc agt tat cgc ttg ggc acc			290
Asp Ser Glu Gly Val Ala Thr Leu Pro Leu Ser Tyr Arg Leu Gly Thr			
80	85	90	
tgg gtg ctg gtc act gct gcc cgc cct ggc ttc ctc acc aac tct gtg			338
Trp Val Leu Val Thr Ala Ala Arg Pro Gly Phe Leu Thr Asn Ser Val			
95	100	105	
ccc tgg cgt gtt gac aag ctg ccc ttg tat gcg tct gtc agc ctc tac			386
Pro Trp Arg Val Asp Lys Leu Pro Leu Tyr Ala Ser Val Ser Leu Tyr			
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ctg ctc cct gag cgg ccg gcc acg ctc atc ctc tat gag gac ctg gtg			434
Leu Leu Pro Glu Arg Pro Ala Thr Leu Ile Leu Tyr Glu Asp Leu Val			
125	130	135	
cac att ctc cta ggc tct ccc ggt gcc cgc tcc cag ccc ttg gtg cag			482
His Ile Leu Leu Gly Ser Pro Gly Ala Arg Ser Gln Pro Leu Val Gln			
140	145	150	155
ttc cag cgc cgg gct gcc cgc ctg cct gtc agc tcc acc tac agc cag			530
Phe Gln Arg Arg Ala Ala Arg Leu Pro Val Ser Ser Thr Tyr Ser Gln			
160	165	170	
ctc tgg gcg tca ctt acg cct gcc agc acc cag cag gaa atg cgg gct			578
Leu Trp Ala Ser Leu Thr Pro Ala Ser Thr Gln Gln Glu Met Arg Ala			
175	180	185	
ttc cct gcc ttc ctg ggc act gag gcc tcc agc tca ggc aat ggc tcc			626
Phe Pro Ala Phe Leu Gly Thr Glu Ala Ser Ser Ser Gly Asn Gly Ser			
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tgg ctg gag ctg atg ccc ctg act gct gtg agc gtg cac ctg ctg aca			674
Trp Leu Glu Leu Met Pro Leu Thr Ala Val Ser Val His Leu Leu Thr			
205	210	215	

gtt aat ggg aca gag gtg ccg ctc tca ggc ccc att cac ctg tcc tgc	722
Gly Asn Gly Thr Glu Val Pro Leu Ser Gly Pro Ile His Leu Ser Leu	
220 225 230 235	
ccc gtg ccc tcc gag act cgt gcc ctc acc gtg ggc acc agc att cca	770
Pro Val Pro Ser Glu Thr Arg Ala Leu Thr Val Gly Thr Ser Ile Pro	
240 245 250	
gcc tgg aga ttt gac ccc aag agt ggg ctg tgg gtg cgc aat ggc act	818
Ala Trp Arg Phe Asp Pro Lys Ser Gly Leu Trp Val Arg Asn Gly Thr	
255 260 265	
gtt gta atc cgg aag gaa ggc cgg cag ctc tac tgg acc ttc gtc tcc	866
Gly Val Ile Arg Lys Glu Gly Arg Gln Leu Tyr Trp Thr Phe Val Ser	
270 275 280	
ccc cag ctg ggg tac tgg gtg gcc gcc atg gcc tcc ccc acg gct ggg	914
Pro Gln Leu Gly Tyr Trp Val Ala Ala Met Ala Ser Pro Thr Ala Gly	
285 290 295	
ctg gtc acc atc acg tcg ggc atc cag gac atc ggc acc tac cac acc	962
Leu Val Thr Ile Thr Ser Gly Ile Gln Asp Ile Gly Thr Tyr His Thr	
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atc ttc ttg ctc acc atc ctg gca gcc ctg gcc ctg ctg gtg ctt atc	1010
Ile Phe Leu Leu Thr Ile Leu Ala Ala Leu Leu Val Leu Ile	
320 325 330	
ctg ctg tgt ctg ctc atc tac tac tgc cgg agg cgc tgc ctg aag ccg	1058
Leu Leu Cys Leu Leu Ile Tyr Tyr Cys Arg Arg Arg Cys Leu Lys Pro	
335 340 345	
agg caa cag cac cgc aag ctg cag ctc tcg ggg ccc tct gac ggt aac	1106
Arg Gln Gln His Arg Lys Leu Gln Leu Ser Gly Pro Ser Asp Gly Asn	
350 355 360	
aaa cga gac cag gcc acc tcg atg tcc cag ctc cac ctc atc tgt ggg	1154
Lys Arg Asp Gln Ala Thr Ser Met Ser Gln Leu His Leu Ile Cys Gly	
365 370 375	
gga ccc ctg gaa ccc gcc ccg tcg ggg gac ccc gag gct ccg cct cca	1202
Gly Pro Leu Glu Pro Ala Pro Ser Gly Asp Pro Glu Ala Pro Pro Pro	
380 385 390 395	

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cg ^g gat gac ttc ttc cgc acc aag cc ^g cgc tct gcc agc cgc cc ^g gcc Arg Asp Asp Phe Phe Arg Thr Lys Pro Arg Ser Ala Ser Arg Pro Ala 415	420	425	1298
gcc gag cct tcg ggt gcc cgc ggg ggc gag agc gcc ggg ctc aag ggc Ala Glu Pro Ser Gly Ala Arg Gly Gly Glu Ser Ala Gly Leu Lys Gly 430	435	440	1346
gct cgc tcg gcc gag ggc ccc ggc ggg ctg gag ccc ggc cta gag gag Ala Arg Ser Ala Glu Gly Pro Gly Gly Leu Glu Pro Gly Leu Glu Glu 445	450	455	1394
cac cgg cgg ggg ccc tcg ggg gct gcg gcc ttc ctg cac gag cc ^g ccc His Arg Arg Gly Pro Ser Gly Ala Ala Ala Phe Leu His Glu Pro Pro 460	465	470	1442
tcg ccg ccg ccc ttc gac cac tac ctg ggc cac aag ggg gcg gcc Ser Pro Pro Pro Pro Phe Asp His Tyr Leu Gly His Lys Gly Ala Ala 480	485	490	1490
gag ggc aag acc ccc gac ttc ctg ctg tcg cag tcg gtg gac cag ctg Glu Gly Lys Thr Pro Asp Phe Leu Leu Ser Gln Ser Val Asp Gln Leu 495	500	505	1538
g ^c g cgg ccg ccg tcg ctg ggc cag g ^c g ggg cag ctc atc ttc tgc ggc Ala Arg Pro Pro Ser Leu Gly Gln Ala Gly Gln Leu Ile Phe Cys Gly 510	515	520	1586
tcc atc gac cac ctc aag gac aac gtc tac cgc aac gtc atg ccc acc Ser Ile Asp His Leu Lys Asp Asn Val Tyr Arg Asn Val Met Pro Thr 525	530	535	1634
ctg gtg atc ccc g ^c g c ^c g tac gtg cgc ctc ggc g ^c g g ^c g ggc g ^c g Leu Val Ile Pro Ala His Tyr Val Arg Leu Gly Gly Glu Ala Gly Ala 540	545	550	1682
gcc ggc gtg ggc gac gag cc ^g gcc cc ^g gag ggc ac ^g gca ccc ggc 1730			

Ala	Gly	Val	Gly	Asp	Glu	Pro	Ala	Pro	Pro	Glu	Gly	Thr	Ala	Pro	Gly	
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Pro	Ala	Arg	Ala	Phe	Pro	Gln	Pro	Asp	Pro	Gln	Arg	Pro	Gln	Met	Pro	
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																585
ggc	cac	tcg	ggc	ccg	ggg	ggc	gag	ggc	ggc	ggg	ggc	ggc	gag	ggc	Gly	1826
Gly	His	Ser	Gly	Pro	Gly											
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tgg	ggg	gcc	ggg	cgc	gct	ccc	gtc	agt	ggc	tca	gtc	acc	atc	cct		1874
Trp	Gly	Ala	Gly	Arg	Ala	Ala	Pro	Val	Ser	Gly	Ser	Val	Thr	Ile	Pro	
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																610
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gtg	cta	tcc	aac	gag	tcc	acc	atg	gct	cag	ctc	aac	ggg	gag	ctg	cag	1922
Val	Leu	Phe	Asn	Glu	Ser	Thr	Met	Ala	Gln	Leu	Asn	Gly	Glu	Leu	Gln	
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gcc	ctg	acc	gag	aag	ctg	ctg	gaa	ctg	ggc	gtg	aag	ccg	cac	ccg		1970
Ala	Leu	Thr	Glu	Lys	Lys	Leu	Leu	Glu	Leu	Gly	Val	Lys	Pro	His		
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cgc	gcc	tgg	ttc	gtg	tcc	ctc	gac	ggg	cgc	tcc	aac	tcg	caa	gtg	cgc	2018
Arg	Ala	Trp	Phe	Val	Ser	Leu	Asp	Gly	Arg	Ser	Asn	Ser	Gln	Val	Arg	
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																665
cac	tct	atc	gac	ctg	cag	gct	ggc	ggc	ggg	gca	cgc	agc	acc	gac		2066
His	Ser	Tyr	Ile	Asp	Leu	Gln	Ala	Gly	Gly	Ala	Arg	Ser	Thr	Asp		
																670
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gcc	agc	ctg	gac	tcg	ggc	gta	gat	gtc	cac	gag	gct	cg	ccc	ggc	cgc	2114
Ala	Ser	Leu	Asp	Ser	Gly	Val	Asp	Val	His	Glu	Ala	Arg	Pro	Ala	Arg	
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cgc	cgg	ccc	gct	agg	gag	gag	cgg	gag	cgc	gcc	ccg	cct	gcc	gct	cgc	2162
Arg	Arg	Pro	Ala	Arg	Glu	Glu	Arg	Glu	Arg	Ala	Pro	Pro	Ala	Ala	Pro	
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																710
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ccg	ccg	ccc	gct	ccc	ccg	ctg	gct	ctc	agc	gag	gac	acg	gag			2210
Pro	Pro	Pro	Pro	Ala	Pro	Pro	Arg	Leu	Ala	Leu	Ser	Glu	Asp	Thr	Glu	
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Pro Ser Ser Ser Glu Ser Arg Thr Gly Leu Cys Ser Pro Glu Asp Asn	
735 740 745	
tcg ctg acg ccg ctg ctg gac gag gtg gcg gcg ccc gag ggc cgg gcg	2306
Ser Leu Thr Pro Leu Leu Asp Glu Val Ala Ala Pro Glu Gly Arg Ala	
750 755 760	
gcc acg gta ccc cgg ggg cgg ggc cgc acg cgc ggg gac agc tcc cgc	2354
Ala Thr Val Pro Arg Gly Arg Ser Arg Gly Asp Ser Ser Arg	
765 770 775	
agc agc gcc agc gag ctg cgg cgc gac tcg ctc acc agc ccg gag gac	2402
Ser Ser Ala Ser Glu Leu Arg Arg Asp Ser Leu Thr Ser Pro Glu Asp	
780 785 790 795	
gag ctg ggg gcg gag gtg ggc gac gag gcg gga gac aag aag agc ccg	2450
Glu Leu Gly Ala Glu Val Gly Asp Glu Ala Gly Asp Lys Lys Ser Pro	
800 805 810	
tgg cag cgg cgg gag gag cgg ccg ctg atg gtg ttc aac gtc aag	2495
Trp Gln Arg Arg Glu Glu Arg Pro Leu Met Val Phe Asn Val Lys	
815 820 825	
tagcgccccgc gcagggcctg gcaccgcgcc tcccgcgccg gcccccaccc agggtgcgcg	2555
ccccgggggc ccgcgggggc cctcgcgct agctcccagc cccaggccgg agaggggccc	2615
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 35 40 45
 Val Ser Gly Glu Leu Val Pro Leu Ala Arg Ala Ser Val Asp Val Phe
 50 55 60
 Gly Asn Arg Thr Leu Leu Ala Ala Gly Thr Thr Asp Ser Glu Gly Val
 65 70 75 80
 Ala Thr Leu Pro Leu Ser Tyr Arg Leu Gly Thr Trp Val Leu Val Thr
 85 90 95
 Ala Ala Arg Pro Gly Phe Leu Thr Asn Ser Val Pro Trp Arg Val Asp
 100 105 110
 Lys Leu Pro Leu Tyr Ala Ser Val Ser Leu Tyr Leu Leu Pro Glu Arg
 115 120 125
 Pro Ala Thr Leu Ile Leu Tyr Glu Asp Leu Val His Ile Leu Leu Gly
 130 135 140
 Ser Pro Gly Ala Arg Ser Gln Pro Leu Val Gln Phe Gln Arg Arg Ala
 145 150 155 160
 Ala Arg Leu Pro Val Ser Ser Thr Tyr Ser Gln Leu Trp Ala Ser Leu
 165 170 175
 Thr Pro Ala Ser Thr Gln Gln Glu Met Arg Ala Phe Pro Ala Phe Leu
 180 185 190
 Gly Thr Glu Ala Ser Ser Ser Gly Asn Gly Ser Trp Leu Glu Leu Met
 195 200 205
 Pro Leu Thr Ala Val Ser Val His Leu Leu Thr Gly Asn Gly Thr Glu
 210 215 220
 Val Pro Leu Ser Gly Pro Ile His Leu Ser Leu Pro Val Pro Ser Glu
 225 230 235 240
 Thr Arg Ala Leu Thr Val Gly Thr Ser Ile Pro Ala Trp Arg Phe Asp
 245 250 255
 Pro Lys Ser Gly Leu Trp Val Arg Asn Gly Thr Gly Val Ile Arg Lys
 260 265 270
 Glu Gly Arg Gln Leu Tyr Trp Thr Phe Val Ser Pro Gln Leu Gly Tyr
 275 280 285
 Trp Val Ala Ala Met Ala Ser Pro Thr Ala Gly Leu Val Thr Ile Thr
 290 295 300
 Ser Gly Ile Gln Asp Ile Gly Thr Tyr His Thr Ile Phe Leu Leu Thr
 305 310 315 320
 Ile Leu Ala Ala Leu Ala Leu Val Leu Ile Leu Leu Cys Leu Leu
 325 330 335
 Ile Tyr Tyr Cys Arg Arg Cys Leu Lys Pro Arg Gln Gln His Arg
 340 345 350

Lys Leu Gln Leu Ser Gly Pro Ser Asp Gly Asn Lys Arg Asp Gln Ala
 355 360 365
 Thr Ser Met Ser Gln Leu His Leu Ile Cys Gly Gly Pro Leu Glu Pro
 370 375 380
 Ala Pro Ser Gly Asp Pro Glu Ala Pro Pro Pro Gly Pro Leu His Ser
 385 390 395 400
 Ala Phe Ser Ser Ser Arg Asp Leu Ala Ser Ser Arg Asp Asp Phe Phe
 405 410 415
 Arg Thr Lys Pro Arg Ser Ala Ser Arg Pro Ala Ala Glu Pro Ser Gly
 420 425 430
 Ala Arg Gly Gly Glu Ser Ala Gly Leu Lys Gly Ala Arg Ser Ala Glu
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 Gly Pro Gly Gly Leu Glu Pro Gly Leu Glu Glu His Arg Arg Gly Pro
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 Ser Gly Ala Ala Ala Phe Leu His Glu Pro Pro Ser Pro Pro Pro Pro
 465 470 475 480
 Phe Asp His Tyr Leu Gly His Lys Gly Ala Ala Glu Gly Lys Thr Pro
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 Asp Phe Leu Leu Ser Gln Ser Val Asp Gln Leu Ala Arg Pro Pro Ser
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 Leu Gly Gln Ala Gly Gln Leu Ile Phe Cys Gly Ser Ile Asp His Leu
 515 520 525
 Lys Asp Asn Val Tyr Arg Asn Val Met Pro Thr Leu Val Ile Pro Ala
 530 535 540
 His Tyr Val Arg Leu Gly Gly Glu Ala Gly Ala Ala Gly Val Gly Asp
 545 550 555 560
 Glu Pro Ala Pro Pro Glu Gly Thr Ala Pro Gly Pro Ala Arg Ala Phe
 565 570 575
 Pro Gln Pro Asp Pro Gln Arg Pro Gln Met Pro Gly His Ser Gly Pro
 580 585 590
 Gly Gly Glu Gly Gly Gly Gly Glu Gly Trp Gly Ala Gly Arg
 595 600 605
 Ala Ala Pro Val Ser Gly Ser Val Thr Ile Pro Val Leu Phe Asn Glu
 610 615 620
 Ser Thr Met Ala Gln Leu Asn Gly Glu Leu Gln Ala Leu Thr Glu Lys
 625 630 635 640
 Lys Leu Leu Glu Leu Gly Val Lys Pro His Pro Arg Ala Trp Phe Val
 645 650 655
 Ser Leu Asp Gly Arg Ser Asn Ser Gln Val Arg His Ser Tyr Ile Asp
 660 665 670
 Leu Gln Ala Gly Gly Gly Ala Arg Ser Thr Asp Ala Ser Leu Asp Ser
 675 680 685

Gly Val Asp Val His Glu Ala Arg Pro Ala Arg Arg Arg Pro Ala Arg
 690 695 700
 Glu Glu Arg Glu Arg Ala Pro Pro Ala Pro Pro Pro Pro Pro Ala
 705 710 715 720
 Pro Pro Arg Leu Ala Leu Ser Glu Asp Thr Glu Pro Ser Ser Ser Glu
 725 730 735
 Ser Arg Thr Gly Leu Cys Ser Pro Glu Asp Asn Ser Leu Thr Pro Leu
 740 745 750
 Leu Asp Glu Val Ala Ala Pro Glu Gly Arg Ala Ala Thr Val Pro Arg
 755 760 765
 Gly Arg Gly Arg Ser Arg Gly Asp Ser Ser Arg Ser Ser Ala Ser Glu
 770 775 780
 Leu Arg Arg Asp Ser Leu Thr Ser Pro Glu Asp Glu Leu Gly Ala Glu
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 Glu Arg Pro Leu Met Val Phe Asn Val Lys
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<211> 2478

<212> DNA

<213> Artificial Sequence

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<223> This is a degenerate sequence that encodes the amino acid sequence of SEQ ID NO:2.

<221> variation

<222> (1)...(2478)

<223> N is any nucleotide.

<400> 3

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athytnatha argtnccargt ntaygtwnsn ggnarytny tnccnytny nmgngcnwsn	180
gtngaygtnt tyggnaaymg nacnytnytn gcngcnggna cnacngayws ngarggngtn	240
gcnacnytnytnytna ymgnytnytn acntgggtnty tnctnacngc ngnmgnccn	300
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 aayggnaacng argtncccnyt nwsnggnccn athcayytnw snytnccngt nccnwsngar 720
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 gtnathccng cncaytaygt nmgnytnngn gngargcng gngcngcngg ntngngngay 1680
 garccngcnc cnccngargg naclgnccn ggnccngcnm gngcnttycc ncacccngay 1740
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 ytnttyaayg arwsnacnat ggcncarytn aayggngary tncargcnyt nacnaraar 1920
 aarytnytn arytngngnt naarcnccay cnmngncnt ggttygtwns nytnayggn 1980
 mgnwsnaayw sncargtnmg ncaywsntay athgayytn argcngngg ngngcnmgn 2040
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 wsngcnwsng arytngmgnmg ngaywsnysytn acnwsnccng argaygaryt ngngcngar 2400
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<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer

<400> 4

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 <211> 291
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<220>
 <223> Expressed sequence tag

<221> variation
 <222> (1)...(1)
 <223> N is any nucleotide.

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cccccccancc	cgcacgagat	cctgatcaag	gtcaggtgt	atgtgagcgg	ggagctggtg	180
cccctggccc	gggcctcact	ggatgtgttt	ggaaaccgga	ctctgctggc	agctggcacc	240
acanactcat	agggtgtggc	ccnccctgcc	cctcagttat	cgcttggca	c	291